

SEQUENCE LISTING

<110> Chambon, Pierre - Metzger, Daniel

<120> Transgenic mouse for targeted recombination mediated by modified Cre-ER

<130> D18961

<150> FR 00 12 570

<151> 2000-10-03

<160> 14

<170> PatentIn Ver. 2.1

<210> I

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1788)

<400> 1

atg acc atg acc ctc cac acc aaa gca tct ggg atg gcc cta ctg cat	48
Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His	
1 5 10 15	

cag atc caa ggg aac gag ctg gag ccc ctg aac cgt ccg cag ctc aag	96
Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys	
20 25 30	

atc ccc ctg gag cgg ccc ctg ggc gag gtg tac ctg gac agc agc aag	144
Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys	
35 40 45	

ccc gcc gtg tac aac tac ccc gag ggc gcc tac gag ttc aac gcc	192
Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala	
50 55 60	

gcc gcc gcc aac gcg cag gtc tac ggt cag acc ggc ctc ccc tac	240
Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr	
65 70 75 80	

ggc ccc ggg tct gag gct gcg ggc ttc ggc tcc aac ggc ctg ggg ggt	288
Gly Pro Gly Ser Gln Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly	
85 90 95	

tcc ccc cca ctc aac agc gtg tct ccg agc ccc ctg atg cta ctg cac	336
Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His	
100 105 110	

ccg ccg ccg dag ctg tcg cct ttc ctg cag ccc cac ggc cag cag gtg	394
Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val	
115 120 125	

ccc tac tac ctg gag aac gag ccc agc ggc tac acg gtg cgc gag gcc	432
Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala	
130 135 140	

ggc ccg ccg gca ttc tac agg cca aat tca gat aat cga cgc cag ggt Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly 145 150 155 160	480
ggc aga gaa aga ttg gcc agt acc aat gac aag gga agt atg gct atg Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met 165 170 175	528
gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat gct Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala 180 185 190	576
tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc ttc Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe 195 200 205	624
tcc aag aga agt att caa gga cat aac gac tat atg tgt cca gcc acc Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr 210 215 220	672
aac cag tgc acc att gat aaa aac agg agg aag agg tgc cag gcc tgc Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys 225 230 235 240	720
cgg ctc cgc aaa tgc tac gaa gtg gga atg atg aaa ggt ggg ata cga Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg 245 250 255	768
aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga gat Lys Asp Arg Arg Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp 260 265 270	816
gat ggg gag ggc agg ggt gaa gtg ggg tct gct gga gac atg aga gct Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala 275 280 285	864
gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag aac Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn 290 295 300	912
agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg ttg Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu 305 310 315 320	960
gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga ccc Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro 325 330 335	1008
tcc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac agg Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg 340 345 350	1056
gag ctg gtt cac atg atc aac tgg gcc aag agg gtg cca ggc ttt gtg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val 355 360 365	1104
gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg cta Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu 370 375 380	1152
gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca ggg	1200

Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly			
385	390	395	400
aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga aaa			1248
Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly Lys			
405	410	415	
tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca tca			1296
Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser			
420	425	430	
tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc ctc			1344
Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu			
435	440	445	
aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc agc			1392
Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser			
450	455	460	
acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg gac			1440
Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp			
465	470	475	
aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg acc			1488
Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr			
485	490	495	
ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc atc ctc tcc			1536
Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser			
500	505	510	
cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc atg			1584
His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met			
515	520	525	
aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg gag atg ctg			1632
Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Glu Met Leu			
530	535	540	
gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc gtg			1680
Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val			
545	550	555	
560			
gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca tcc			1728
Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser			
565	570	575	
cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc oct			1776
His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro			
580	585	590	
gcc aca gtc tga			1788
Ala Thr Val			
595			

<210> 2
<211> 595
<212> PRT
<213> Homo sapiens

<400> 2

Met	Thr	Met	Thr	Leu	His	Thr	Lys	Ala	Ser	Gly	Met	Ala	Leu	Leu	His
1				5										10	15
Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys															
				20			25							30	
Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys															
				35			40							45	
Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala															
				50			55							60	
Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr															
				65			70							75	80
Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly															
				85			90							95	
Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His															
				100			105							110	
Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Cln Val															
				115			120							125	
Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala															
				130			135							140	
Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly															
				145			150							155	160
Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met															
				165			170							175	
Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala															
				180			185							190	
Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe															
				195			200							205	
Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr															
				210			215							220	
Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys															
				225			230							235	240
Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg															
				245			250							255	
Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp															
				260			265							270	
Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala															
				275			280							285	
Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn															
				290			295							300	
Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu															
				305			310							315	320

Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
 325 330 335
 Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
 340 345 350
 Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
 355 360 365
 Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
 370 375 380
 Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly
 385 390 395 400
 Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly Lys
 405 410 415
 Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
 420 425 430
 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
 435 440 445
 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
 450 455 460
 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
 465 470 475 480
 Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
 485 490 495
 Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
 500 505 510
 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
 515 520 525
 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
 530 535 540
 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
 545 550 555 560
 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
 565 570 575
 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
 580 585 590
 Ala Thr Val
 595

<210> 3
 <211> 1983
 <212> DNA
 <213> Artificial sequence

<220>
<221> CDS
<222> (1)..(1983)

<220>
<223> Chimeric sequence Homosapiens-Bacteriophage PI

<400> 3						
atg tcc aat tta ctg acc gta cac caa aat ttg cct gca tta ccg gtc	48					
Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val						
1	5	10	15			
gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg	96					
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg						
20	25	30				
gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt	144					
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val						
35	40	45				
tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt	192					
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe						
50	55	60				
ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gtc	240					
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Tyr Leu Gln Ala						
65	70	75	80			
cgc ggl ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac	288					
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn						
85	90	95				
atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct	336					
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala						
100	105	110				
gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt	384					
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly						
115	120	125				
gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag	432					
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln						
130	135	140				
gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat	480					
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn						
145	150	155	160			
ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa	528					
Ieu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu						
165	170	175				
att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga	576					
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg						
180	185	190				
atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt	624					
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly						
195	200	205				
gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg	672					

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp			
210	215	220	
att tcc gtc tct ggt gta gct gat gat ccg aat aac tac ctg ttt tgc			720
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys			
225	230	235	240
cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta			768
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu			
245	250	255	
tca act cgc gcc ctg qaa ggg att ttt gaa gca act cat cga ttg att			816
Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Tle			
260	265	270	
tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga			864
Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly			
275	280	285	
cac agt gcc cgt gtc gga gcc gcg cga gat atg gac agc gct gga gtt			912
His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val			
290	295	300	
tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att			950
Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile			
305	310	315	320
gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg			1008
Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val			
325	330	335	
cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga			1056
Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg			
340	345	350	
gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag			1104
Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys			
355	360	365	
aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg			1152
Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu			
370	375	380	
ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga			1200
Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg			
385	390	395	400
ccc ttc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac			1248
Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp			
405	410	415	
agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca ggc ttt			1296
Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe			
420	425	430	
gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg			1344
Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp			
435	440	445	
cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca			1392
Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro			

450	455	460	
ggg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly 465 470 475 480			1440
aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr 485 490 495			1488
tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys 500 505 510			1536
ctc aaa tat att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser 515 520 525			1584
agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu 530 535 540			1632
gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu 545 550 555 560			1680
acc ctg cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu 565 570 575			1728
tcc cac atc agg cac atg agt aac aaa aga atg gag cat ctg tac agc Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser 580 585 590			1776
atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag atg Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Glu Met 595 600 605			1824
ctg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser 610 615 620			1872
gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser 625 630 635 640			1920
tcc cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe 645 650 655			1968
cct gcc aca gtc tga Pro Ala Thr Val 660			1983

<210> 4
<211> 660
<212> PRT
<213> Artificial sequence
<223> Chimeric sequence Homosapiens-Bacteriophage P1

<400> 4
Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255
Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
260 265 270
Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
275 280 285
His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300
Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
340 345 350

Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
355 360 365

Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
370 375 380

Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
385 390 395 400

Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
405 410 415

Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
420 425 430

Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
435 440 445

Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
450 455 460

Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly
465 470 475 480

Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
485 490 495

Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
500 505 510

Leu Lys Ser Ile Ile Leu Leu Asn Ser GLy Val Tyr Thr Phe Leu Ser
515 520 525

Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
530 535 540

Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
545 550 555 560

Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
565 570 575

Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser
580 585 590

Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met
595 600 605

Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
610 615 620

Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
625 630 635 640

Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe

645

650

655

Pro Ala Thr Val
660

<210> 5
<211> 1983
<212> DNA
<213> Artificial sequence

<220>
<221> CDS
<222> (1)..(1983)

<220>
<223> Chimeric sequence Homosapiens-Bacteriophage Pl

```

<400> 5
atg tcc aat tta ctg acc gta cac caa aat ttg cct gca tta ccg gtc 48
Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
    1           5           10          15

```

gat gca acg act gat gag gtt cgc aag aac ctg atg gac atg ttc agg 96
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144
 Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt 192
 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

ccc gca gaa cct gaa gat gtt cg^c gat tat ctt cta tat ctt cag gcg 240
 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288
 Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct 336
 Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 . 110

gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt 384
 Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Ash Val Asp Ala Gly
 115 120 125

gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag 432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat 480
 Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa 528

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga 576
 Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190

atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt 624
 Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205

gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg 672
 Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
 210 215 220

att tcc gtc tct ggt gta gct gat gat ccg aat aac tac ctg ttt tgc 720
 Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240

cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta 768
 Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
 245 250 255

tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att 816
 Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270

tac ggc gct aag gat gac tct ggt cay aga tac ctg gcc tgg tct gga 864
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285

cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt 912
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300

tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att 960
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320

gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg 1008
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335

cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga 1056
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
 340 345 350

gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag 1104
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
 355 360 365

aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg 1152
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
 370 375 380

ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga 1200
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
 385 390 395 400

ccc ttc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac 1248
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp

405	410	415	
agg gag ctg gtt cac atg atc aac ttg gcg aag agg gtg cca ggc ttt Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe			1296
420	425	430	
gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp			1344
435	440	445	
cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro			1392
450	455	460	
gtg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly			1440
465	470	475	480
aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr			1488
485	490	495	
tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys			1536
500	505	510	
ctc aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser			1584
515	520	525	
agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu			1632
530	535	540	
gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu			1680
545	550	555	560
acc ctg cag cag cac cag cgg ctg gcc cag ctc ctc atc ctc Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Ile Leu			1728
565	570	575	
tcc cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser			1776
580	585	590	
atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg gag gcg Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Glu Ala			1824
595	600	605	
gcg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser			1872
610	615	620	
gtg gag gag acc gac caa agc cac ttg gcc act ggc ggc tct act tca Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser			1920
625	630	635	640
tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe			1968
645	650	655	

cct gcc aca gct tga 1983
 Pro Ala Thr Ala
 660

<210> 6
<211> 660
<212> PRT
<213> Artificial sequence
<223> Chimeric sequence Homosapiens-Bacteriophage PI

<400> 6
Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
340 345 350

Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
355 360 365

Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
370 375 380

Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
385 390 395 400

Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
405 410 415

Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
420 425 430

Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
435 440 445

Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
450 455 460

Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly
465 470 475 480

Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
485 490 495

Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
500 505 510

Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser
515 520 525

Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
530 535 540

Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
545 550 555 560

Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Ile Leu
565 570 575

Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser

580

585

590

Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala
 595 600 605

Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620

Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655

Pro Ala Thr Ala
 660

<210> 7

<211> 1983

<212> DNA

<213> Artificial sequence

<220>

<221> CDS

<222> (1)..(1983)

<220>

<223> Chimeric sequence Homosapiens-Bacteriophage PI

<400> 7

atg tcc aat tta ctg acc gta cac caa aat ttg cct gca tta ccg gtc 48
 Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15

gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg 96
 Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30

gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144
 Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt 192
 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ott cag gcg 240
 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288
 Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct 336
 Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt 384

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly			
115	120	125	
gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag	432		
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln			
130	135	140	
gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat	480		
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn			
145	150	155	160
ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa	528		
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu			
165	170	175	
att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga	576		
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg			
180	185	190	
atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt	624		
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly			
195	200	205	
gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg	672		
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp			
210	215	220	
att tcc gtc tct ggt gta gct gat gat ccg aat aac tac ctg ttt tgc	720		
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys			
225	230	235	240
cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta	768		
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu			
245	250	255	
tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att	816		
Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile			
260	265	270	
tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga	864		
Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly			
275	280	285	
cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt	912		
His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val			
290	295	300	
tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att	960		
Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile			
305	310	315	320
gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg	1008		
Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val			
325	330	335	
cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga	1056		
Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg			
340	345	350	
gct gcc aac ctt tgg cca aag ccg ctc atg atc aaa cgc tct aag aag	1104		
Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys			

355	360	365	
aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu 370	375	380	1152
ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg 385	390	395	1200
ccc ttc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp 405	410	415	1248
agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca ggc ttt Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe 420	425	430	1296
gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp 435	440	445	1344
cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro 450	455	460	1392
ggg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly 465	470	475	1440
aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr 485	490	495	1488
tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Phe Val Cys 500	505	510	1536
ctc aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser 515	520	525	1584
agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu 530	535	540	1632
gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu 545	550	555	1680
acc ctg cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Ile Leu 565	570	575	1728
tcc cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser 580	585	590	1776
atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag gcg Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Glu Ala 595	600	605	1824

gct gac gcc cac cgc cta cat gct ccc act agc cgt gga ggg gca tcc 1872
 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620

gtg gag gag acg gac caa agc cac ttg gcc act gct ggc tct act tca 1920
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc 1968
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655

cct gcc aca gct tga 1983
 Pro Ala Thr Ala
 660

<210> 8

<211> 660

<212> PRT

<213> Artificial sequence

<223> Chimeric sequence Homosapiens-Bacteriophage P1

<400> 8

Met	Ser	Asn	Leu	Leu	Thr	Val	His	Gln	Asn	Leu	Pro	Ala	Leu	Pro	Val
1															

5

10

15

Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg

20

25

30

Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val

35

40

45

Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe

50

55

60

Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala

65

70

75

80

Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn

85

90

95

Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala

100

105

110

Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly

115

120

125

Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln

130

135

140

Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn

145

150

155

160

Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu

165

170

175

Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg

180

185

190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
340 345 350

Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
355 360 365

Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
370 375 380

Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
385 390 395 400

Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
405 410 415

Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
420 425 430

Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
435 440 445

Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
450 455 460

Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly
465 470 475 480

Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
485 490 495

Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
500 505 510

Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser

515	520	525
Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu		
530	535	540
Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu		
545	550	555
Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu		
565	570	575
Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser		
580	585	590
Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala		
595	600	605
Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser		
610	615	620
Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser		
625	630	635
Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe		
645	650	655
Pro Ala Thr Ala		
660		

<210> 9
<211> 20
<212> DNA
<213> Homo sapiens

<400> 9
tccttcacca agcacatctg

20

<210> 10
<211> 20
<212> DNA
<213> Homo sapiens

<400> 10
tgcagccctc acaactgtat

20

<210> 11
<211> 21
<212> DNA
<213> Homo sapiens

<400> 11
caaacctgcac ttgtcactta g

21

<210> 12
<211> 20
<212> DNA

<213> Homo sapiens

<400> 12

atgtttcata gttggatatac

20

<210> 13

<211> 37

<212> DNA

<213> Mus musculus

<400> 13

atacgcggcc gcgaattcca gcaggaatca ggttagct

37

<210> 14

<211> 37

<212> DNA

<213> Mus musculus

<400> 14

atacgccggc cgctgcagca caggagggtg ctatgag

37